

F1: ASTLGSSTPKVDNAKPFQPPREHVHVQVTH^S_XMPPQKIEIFKSIEG^W_RAEQNILV^H_FLKPVEKWCWQ
 F2: DFLPDDP^S_TEGFDEQVKELRARAKEIPDDYFVVVLVGDMITEEALPTYOTMLNTILDGV
 F3: DETGASLTPWAVWT
 F4: DLLHTYLYLSGRV
 F5: DMRQIQKTIQYLI
 F6: TENSPYLGFIYTSFQER
 F7: DV^K_FLAQI^C_QGTIASDEKRRHETAYTKIVEKLFEIDPDGTVLAFADMMRKKI^S_TMPAHLMY
 F8: DNLF
 F9: dvFLAV^A_IQRL^G_IVYTAK
 F10: DYADILEFLVGRWK
 F11: VADLTGLSGEGRKA^Q_GDYVCGLPPIRRIRLEERAQGRAKEGPVVPFSWIFDRQVKL

FIGURE 1

10

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HindIII

1 GCTCACTTGTGTGGAGGAGAAAAACAGAACTCACAAAAAGCTTTGCGACTGCCAAGAACAACAACA 69
42

70 ACAACAAGATCAAGAAGAAGAAGATCAAAAATGGCTCTTCTGAATCACTCCAGTGACCTTGCAA 138
METAlaLeuArgIleThrProValThrLeuGln

EcoRV

BglII

NcoI

139 TCGGAGAGATATCGTTTCGTTTCCTAAGAAGGCTAATCTCAGATCTCCCAAATTCGCCCATGGCC 207
SerGluArgTyrArgSerPheSerPheProLysLysAlaAsnLeuArgSerProLysPheAlaMETAla
149 185 201

HindII

208 TCCACCCCTCGGATCATCCACACCGAAGGTTGACAAATGCCAAGAAGCCTTTTCAACCTCCACGAGAGGTT 276
SerThrLeuGlySerSerThrProLysValAspAsnAlaLysLysProPheGlnProProArgGluVal
238

277 CATGTTCAGGTGACGCCACTCCATGCCACCACAGAAAGATAGAGATTTTCAAATCCATCGAGGTTGGGCT 345
HisValGlnValThrHisSerMETProProGlnLysIleGluIlePheLysSerIleGluGlyTrpAla

346 GAGCAGAACATATTGGTTCACCTAAAGCCAGTGGAGAAATGTTGGCAAGCACAGGATTCTTGCCGGAC 414
GluGlnAsnIleLeuValHisLeuLysProValGluLysCysTrpGlnAlaGlnAspPheLeuProAsp

FIGURE 2

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415	CCTGCATCTGAAGGATTTTGATGAACAAGTCAAGGAACCTAAGGGCAAGAGCAAAAGAGATTTCCTGATGAT	483
	ProAlaSerGluGlyPheAspGluGlnValLysGluLeuArgAlaArgAlaLysGluIleProAspAsp	
484	TACTTTGTGTTTGGTTGGAGATATGATTACAGAGGAAGCCCTACCTACTTACCAAAACAATGCTTTAAT	552
	TyrPheValValLeuValGlyAspMETIleThrGluGluAlaLeuProThrTyrGlnThrMETLeuAsn	
553	ACCCTAGATGGTGTAAGTACGATGAGACTGGGGCTAGCCCTTACGCCTTGGGCTGTCTGGACTAGGGCTTGG	621
	ThrLeuAspGlyValArgAspGluThrGlyAlaSerLeuThrProTrpAlaValTrpThrArgAlaTrp	
	PvuII	AccI
622	ACAGCTGAAGAGAACAGGCATGGCGATCTTCTCCACACCTATCTCTACCTTTCTGGCGGGTAGACATG	690
	ThrAlaGluGluAsnArgHisGlyAspLeuLeuHisThrTyrLeuTyrLeuSerGlyArgValAspMET	
	626	684
	BamHI	
691	AGGCAGATACAGAAGACAATTTCAGTATCTCATTTGGGTCAGGAATGGATCCTCTGACCGAAAACAGCCCC	759
	ArgGlnIleGlnLysThrIleGlnTyrLeuIleGlySerGlyMETAspProArgThrGluAsnSerPro	
	736	
760	TACCTTGGGTTTCATCTACACATCGTTTCAAGAGCGTGCCACATTTGTTTCTACCGGAAACACCGCCAGG	828
	TyrLeuGlyPheIleTyrThrSerPheGlnGluArgAlaThrPheValSerHisGlyAsnThrAlaArg	

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SphI

|

829 CATGCAAGGATCATGGGACGTGAAACTGGCGCAAAATTTGTGTACAAATCGCGTCTGACGAAAAGCGT 897
HisAlaLysAspHisGlyAspValLysLeuAlaGlnIleCysGlyThrIleAlaSerAspGluLysArg
833

Clal

|

898 CACGAGACCGCTTATACAAAGATAGTCGAAAAGCTATTCGAGATCGATCCTGATGGCACCGTTCTTGCT 966
HisGluThrAlaTyrThrLysIleValGluLysLeuPheGluIleAspProAspGlyThrValLeuAla
942

BglII

|

967 TTTGCCGACATGATGAGGAAAAGATCTCGATGCCCGCACACTTGATGTACGATGGGCGTGATGACAAC 1035
PheAlaAspMETMETArgLysLysIleSerMETProAlaHisLeuMETTyrAspGlyArgAspAspAsn
990

AccI

|

1036 CTCTTCGAACATTTCTCGGCGGTTGCCCAAGACTCGGCGTCTACACCGCCAAAGACTACGCCGACATA 1104
LeuPheGluHisPheSerAlaValAlaGlnArgLeuGlyValTyrThrAlaLysAspTyrAlaAspIle
1077

1105 CTGGAATTTCTGGTCGGCGGTGGAAAGTGGCGGATTTGACCGGCCCTATCTGGTGAAGGGCGTAAAGCG 1173
LeuGluPheLeuValGlyArgTrpLysValAlaAspLeuThrGlyLeuSerGlyGlyArgLysAla

FIGURE 2

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SacI

|

1174 CAAGATTATGTTTGGGGTTCACCAAGAATCAGAAGGCTGGAGAGAGAGCTCAAGGGCGAGCAAAG 1242
GlnAspTyrValCysGlyLeuProProArgIleArgArgLeuGluGluArgAlaGlnGlyArgAlaLys
1228

PvuII

|

1243 GAAGGACCTGTTGTTCCATTTCAGCTGGATTTTCGATAGACAGGTGAAGCTGTGAAGAAAAAAACGA 1311
GluGlyProValValProPheSerTrpIlePheAspArgGlnValLysLeu
1266

1312 GCAGTGAGTTCGGTTTCTGTTGGCTTATTGGGTAGAGGTTAAACCTATTTTAGATGCTGTTCGTGT 1380

1381 AATGTGGTTTTTTTTTCTTAATCTGAATCTGGTATTGTGTCGTTGAGTTCGCGTGTGTAAACTTG 1449

1450 TGTGGCTGTGGACATATTATAGAACTCGTTATGCCAAATTTTGATGACGGTGGTTATCGTCTCCCCCTGGT 1518

1519 GTTTTTTTTATTGTTT 1533

1 AAAAGAAAAGGTAAGAAAAAACAATGGCTCTCAAGCTCAATCCTTTCTCTCAAAACCCAAAAGT 69
METAlaLeuLysLeuAsnProPheLeuSerGlnThrGlnLysL

BglII

70 TACCTTCTTTTCGCTCTTCCACCAATGGCCAGTACCAGATCTCCTAAGTTCTACATGGCCTCTACCCCTCA 138
euProSerPheAlaLeuProProMETAlaSerThrArgSerProLysPheTyrMETAlaSerThrLeuL

139 AGTCTGGTTCTAAGGAAGTTGAGAAATCTCAAGAAGCCTTTTCATGCCCTCCGCGAGGTACATGTTTCAGG 207
ysSerGlySerLysGluValGluAsnLeuLysLysProPheMETProProArgGluValHisValGlnV

208 TTACCCATTCTATTGCCA 225
alThrHisSerIleAla

FIGURE 3A

AAAAGAAAAA GGTAAGAAAA AAAACA ATG GCT CTC AAG CTC AAT CCT TTC CTT TCT	56
MET Ala Leu Lys Leu Asn Pro Phe Leu Ser	
CAA ACC CAA AAG TTA CCT TCT TTC GCT CTT CCA CCA ATG GCC AGT ACC AGA TCT	110
Gln Thr Gln Lys Leu Pro Ser Phe Ala Leu Pro Pro MET Ala Ser Thr Arg Ser	
CCT AAG TTC TAC ATG GCC TCT ACC CTC AAG TCT GGT TCT AAG GAA GTT GAG AAT	164
Pro Lys Phe Tyr MET Ala Ser Thr Leu Lys Ser Gly Ser Lys Glu Val Glu Asn	
CTC AAG AAG CCT TTC ATG CCT CCT CGG GAG GTA CAT GTT CAG GTT ACC CAT TCT	218
Leu Lys Lys Pro Phe MET Pro Pro Arg Glu Val His Val Thr His Ser	
ATG CCA CCC CAA AAG ATT GAG ATC TTT AAA TCC CTA GAC AAT TGG GCT GAG GAG	272
MET Pro Pro Gln Lys Ile Glu Ile Phe Lys Ser Leu Asp Asn Trp Ala Glu Glu	
AAC ATT CTG GTT CAT CTG AAG CCA GAT GAG AAA TGT TGG CAA CCG CAG GAT TTT	326
Asn Ile Leu Val His Leu Lys Pro Val Glu Lys Cys Trp Gln Pro Gln Asp Phe	
TTG CCA GAT CCC GCC TCT GAT GAT GGA TTT GAT GAG CAA GTC AGG GAA CTC AGG GAG	380
Leu Pro Asp Pro Ala Ser Asp Gly Phe Asp Glu Gln Val Arg Glu Leu Arg Glu	
AGA GCA AAG GAG ATT CCT GAT GAT TAT TTT GTT GTT TTG GGA GAC ATG ATA	434
Arg Ala Lys Glu Ile Pro Asp Asp Tyr Phe Val Val Leu Val Gly Asp MET Ile	
ACG GAA GAA GCC CTT CCC ACT TAT CAA ACA ATG CTG AAT ACC TTG GAT GGA GTT	488
Thr Glu Glu Ala Leu Pro Thr Tyr Gln Thr MET Leu Asn Thr Leu Asp Gly Val	

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CGG GAT GAA ACA GGT GCA AGT CCT ACT TCT TGG GCA ATT TGG ACA AGG GCA TGG	542
Arg Asp Glu Thr Gly Ala Ser Pro Thr Ser Trp Ala Ile Trp Thr Arg Ala Trp	
ACT GCG GAA GAG AAT AGA CAT GGT GAC CTC CTC AAT AAG TAT CTC TAC CTA TCT	596
Thr Ala Glu Glu Asn Arg His Gly Asp Leu Leu Asn Lys Tyr Leu Tyr Leu Ser	
GGA CGA GTG GAC ATG AGG CAA ATT GAG AAG ACA ATT CAA TAT TTG ATT GGT TCA	650
Gly Arg Val Asp MET Arg Gln Ile Glu Lys Thr Ile Gln Tyr Leu Ile Gly Ser	
GGA ATG GAT CCA CGG ACA GAA AAC AGT CCA TAC CTT GGG TTC ATC TAT ACA TCA	704
Gly MET Asp Pro Arg Thr Glu Asn Ser Pro Tyr Leu Gly Phe Ile Tyr Thr Ser	
TTC CAG GAA AGG GCA ACC TTC ATT TCT CAT GGG AAC ACT GCC CGA CAA GCC AAA	758
Phe Gln Glu Arg Ala Thr Phe Ile Ser His Gly Asn Thr Ala Arg Gln Ala Lys	
GAG CAT GGA GAC ATA AAG TTG GCT CAA ATA TGT GGT ACA ATT GCT GCA GAT GAG	812
Glu His Gly Asp Ile Lys Leu Ala Gln Ile Cys Gly Thr Ile Ala Ala Asp Glu	
AAG CGC CAT GAG ACA GCC TAC ACA AAG ATA GTG GAA AAA CTC TTT GAG ATT GAT	866
Lys Arg His Glu Thr Ala Tyr Thr Lys Ile Val Glu Lys Leu Phe Glu Ile Asp	
CCT GAT GGA ACT GTT TTG GCT TTT GCT GAT ATG ATG AGA AAG AAA ATT TCT ATG	920
Pro Asp Gly Thr Val Leu Ala Phe Ala Asp MET MET Arg Lys Ile Ser MET	
CCT GCA CAC TTG ATG TAT GAT GGC CGA GAT GAT AAT CTT TTT GAC CAC TTT TCA	974
Pro Ala His Leu MET Tyr Asp Gly Arg Asp Asp Asn Leu Phe Asp His Phe Ser	

GCT GTT GCG CAG CAG CGT CTT GGA GTC TAC ACA GCA AAG GAT TAT GCA GAT ATA TTG	1028
Ala Val Ala Gln Arg Leu Gly Val Tyr Thr Ala Lys Asp Tyr Ala Asp Ile Leu	
GAG TTC TTG GTG GGC AGA TGG AAG GTG GAT AAA CTA ACG GGC CTT TCA GCT GAG	1082
Glu Phe Leu Val Gly Arg Trp Lys Val Asp Lys Leu Thr Gly Leu Ser Ala Glu	
GGA CAA AAG GCT CAG GAC TAT GTT TGT CGG TTA CCT CCA AGA ATT AGA AGG CTG	1136
Gly Gln Lys Ala Gln Asp Tyr Val Cys Arg Leu Pro Pro Arg Ile Arg Arg Leu	
GAA GAG AGA GCT CAA GGA AGG GCA AAG GAA GCA CCC ACC ATG CCT TTC AGC TGG	1190
Glu Glu Arg Ala Gln Gly Arg Ala Lys Glu Ala Pro Thr MET Pro Phe Ser Trp	
ATT TTC GAT AGG CAA GTG AAG CTG TAGGTGGCTA AAGTGCAGGA CGAAACCGAA ATGGTTAGTT	1254
Ile Phe Asp Arg Gln Val Lys Leu	
TCACTCTTTT TCATGCCCAT CCCTGCAGAA TCAGAAGTAG AGGTAGAATT TTGTAGTTGC TTTTTTATTA	1324
CAAGTCCAGT TTAGTTAAG GTCTGTGGAA GGGAGTTAGT TGAGGAGTGA ATTTAGTAAG TTGTAGATAC	1394
AGTTGTTTCT TGTGTTGTCA TGAGTATGCT GATAGAGAGC AGCTGTAGTT TTGTTGTTGT GTTCTTTTAT	1464
ATGGTCTCTT GTATGAGTTT CTTTTCTTTC CTTTTCTTCT TTCCCTTTCCCT CTCTCTCTCT CTCTCTCTCT	1534
CTCTTTTCT CTTATCCCAA GTGTCTCAAG TATAATAAGC AAACGATCCA TGTGGCAATT TTGATGATGG	1604
TGATCAGTCT CACAACCTGA TCTTTTGTCT TCTATTGGAA ACACAGCCTG CTTGTTTGAA AAAA	1668

FIGURE 3B

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PCGN3235

1 TGAGAGATAGTGTGAGAGCATTAGCCTTAGAGAGAGAGAGAGAGAGCTTGTGTCTGAAAGAATCCACAA 69

HindIII

70 ATGGCATTGAAGCTTAACCCCTTTGGCATCTCAGCCTTACAACCTTCCCT 117
METAlaLeuLysLeuAsnProLeuAlaSerGlnProTyrAsnPhePro

FIGURE 4A

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PCGN3236

PstI

|

1 ACTTCATGGGCTATTGGACAAGAGCTTGGACTGCAGAAAGAGAACCGACACGGTGATCTTCTCAATAAG 69
ThrSerTrpAlaIleTrpThrArgAlaTrpThrAlaGluGluAsnArgHisGlyAspLeuLeuAsnLys

70 TATCTTTACTTGTCTGGACGCTGTGACATGAGGCAGATTGAAAAGACCACTTCAGTACTTGATTGGTTCT 138
TyrLeuTyrLeuSerGlyArgValAspMETArgGlnIleGluLysThrIleGlnTyrLeuIleGlySer

BamHI

|

139 GGAATGGATCCTAGAACACAGAGAACAAATCCTTACCTCGG 176
GlyMETAspProArgThrGluAsnAsnProTyrLeuAla

FIGURE 4B

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PCGN3235

TGAGAGATAG TGTGAGAGCA TTAGCCTTAG AGAGAGAGAG AGAGAGCTTG TGTCTGAAAG AATCCACAA

ATG GCA TTG AAG CTT AAC CCT TTG GCA TCT CAG CCT TAC AAC TTC CCT TCC TCG
MET Ala Leu Lys Leu Asn Pro Leu Ala Ser Gln Pro Tyr Asn Phe Pro Ser Ser

GCT CGT CCG CCA ATC TCT ACT TTC AGA TCT CCC AAG TTC CTC TGC CTC GCT TCT
Ala Arg Pro Pro Ile Ser Thr Phe Arg Ser Pro Lys Phe Leu Cys Leu Ala Ser

TCT TCT CCC GCT CTC AGC TCC AAG GAG GTT GAG AGT TTG AAG AAG CCA TTC ACA
Ser Ser Pro Ala Leu Ser Ser Lys Glu Val Glu Ser Leu Lys Pro Phe Thr

CCA CCT AAG GAA GTG CAC GTT CAA GTC CTG CAT TCC ATG CCA CCC CAG AAG ATC
Pro Pro Lys Glu Val His Val Gln Val Leu His Ser MET Pro Pro Gln Lys Ile

GAG ATC TTC AAA TCC ATG GAC TGG GCC GAG CAG AAC CTT CTA ACT CAG CTC
Glu Ile Phe Lys Ser MET Glu Asp Trp Ala Glu Gln Asn Leu Thr Gln Leu

AAA GAC GTG AAG TCG TGG CAG CCC CAG GAC TTC TTA CCC GAC CCT GCA TCC
Lys Asp Val Glu Lys Ser Trp Gln Pro Gln Asp Phe Leu Pro Asp Pro Ala Ser

GAT GGG TTC GAA GAT CAG GTT AGA GAG CTA AGA GAG AGG GCA AGA GAG CTC CCT
Asp Gly Phe Glu Asp Gln Val Arg Glu Leu Arg Glu Ala Arg Glu Leu Pro

GAT GAT TAC TTC GTT GTT CTG GTG GGA GAC ATG ATC ACG GAA GAG GCG CTT CCG
Asp Asp Tyr Phe Val Val Leu Val Gly Asp MET Ile Thr Glu Glu Ala Leu Pro

ACC TAT CAA ACC ATG TTG AAC ACT TTG GAT GGA GTG AGG GAT GAA ACT GGC GCT
Thr Tyr Gln Thr MET Leu Asn Thr Leu Asp Gly Val Arg Asp Glu Thr Gly Ala

AGC CCC ACT TCA TGG GCT ATT TGG ACA AGA GCT TGG ACT GCA GAA GAG AAC CGA
Ser Pro Thr Ser Trp Ala Ile Trp Thr Arg Ala Trp Thr Ala Glu Glu Asn Arg

CAC GGT GAT CTT CTC AAT AAG TAT CTT TAC TTG TCT GGA CGT GTT GAC ATG AGG
His Gly Asp Leu Leu Asn Lys Tyr Leu Tyr Tyr Ser Gly Arg Val Asp MET Arg

CAG ATT GAA AAG ACC ATT CAG TAC TTG ATT GGT TCT GGA ATG GAT CCT AGA ACA
Gln Ile Glu Lys Thr Ile Gln Tyr Leu Ile Gly Ser Gly MET Asp Pro Arg Thr

GAG AAC AAT CCT TAC CTC GGC TTC ATC TAC ACT TCA TTC CAA GAA AGA GCC ACC
Glu Asn Asn Pro Tyr Leu Gly Phe Ile Tyr Thr Ser Phe Gln Glu Arg Ala Thr

TTC ATC TCT CAC GGA AAC ACA GCT CGC CAA GCC AAA GAG CAC GGA GAC CTC AAG
Phe Ile Ser His Gly Asn Thr Ala Arg Gln Ala Lys Glu His Gly Asp Leu Lys

CTA GCC CAA ATC TGC GGC ACA ATA GCT GCA GAC GAG AAG CGT CAT GAG ACA GCT
Leu Ala Gln Ile Cys Gly Thr Ile Ala Ala Asp Glu Lys Arg His Glu Thr Ala

TAC ACC AAG ATA GTT GAG AAG CTC TTT GAG ATT GAT CCT GAT GGT ACT GTG ATG
Tyr Thr Lys Ile Val Glu Lys Leu Phe Glu Ile Asp Pro Asp Gly Thr Val MET

GCG TTT GCA GAC ATG ATG AGG AAG AAA ATC TCG ATG CCT GCT CAC TTG ATG TAC
Ala Phe Ala Asp MET MET Arg Lys Lys Ile Ser MET Pro Ala His Leu MET Tyr

GAT GGG CGG GAT GAA AGC CTC TTT GAC AAC TTC TCT TCT GTT GCT CAG AGG CTC
 Asp Gly Arg Asp Glu Ser Leu Phe Asp Asn Phe Ser Ser Val Ala Gln Arg Leu
 GGT GTT TAC ACT GCC AAA GAC TAT GCG GAC ATT CTT GAG TTT TTG GTT GGG AGG
 Gly Val Tyr Thr Ala Lys Asp Tyr Ala Asp Ile Leu Glu Phe Leu Val Gly Arg
 TGG AAG ATT GAG AGC TTG ACC GGG CTT TCA GGT GAA AAC AAA GCG CAA GAG
 Trp Lys Ile Glu Ser Leu Thr Gly Leu Ser Gly Glu Asn Lys Ala Gln Glu
 TAC TTG TGT GGG TTG ACT CCA AGA ATC AGG AGG TTG GAT GAG AGA GCT CAA GCA
 Tyr Leu Cys Gly Leu Thr Pro Arg Ile Arg Arg Leu Asp Glu Arg Ala Gln Ala
 AGA GCC AAG AAA GGA CCC AAG GTT CCT TTC AGC TGG ATA CAT GAC AGA GAA GTG
 Arg Ala Lys Lys Gly Pro Lys Val Pro Phe Ser Trp Ile His Asp Arg Glu Val
 CAG CTC TAA AAAGGAA CAAAGCTATG AAACCTTTTC ACTCTCCGTC GTCCCTCATT TGATCTATCT
 Gln Leu *
 GCTCTTGAAA TTGGTGTAGA TTA CTATGTTT TTTGATATT GTTCGTGGGT CTAGTTACAA AGTTGAGAAG
 CAGTGATTTA GTAGCTTTGT TGTTC CAGT CTTTAAATGT TTTTGTGTTT GGTCCTTTTA GTAAACTTGT
 TGTAGTTAAA TCAGTTGAAC TGTTTGGTCT GT

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GAT	GCC	AAA	ANG	CCT	CAC	ATG	CCT	CCT	AGA	GAA	GCT	CAT	GTG	CAA	AAG	48
Asp	Ala	Lys	Xaa	Pro	His	MET	Pro	Pro	Arg	Glu	Ala	His	Val	Gln	Lys	
1				5					10					15		
ACC	CAT	TCA	ATK	CCG	CCT	CAA	AAG	ATT	GAG	ATT	TTC	AAA	TCC	TTG	GAG	96
Thr	His	Ser	Xaa	Pro	Pro	Gln	Lys	Ile	Glu	Ile	Phe	Lys	Ser	Leu	Glu	
				20				25					30			
GGT	TGG	GCT	GAG	GAG	AAT	GTC	TTG	GTG	CAT	CTT	AAA	CCT	GTG	GAG	AA	143
Gly	Trp	Ala	Glu	Glu	Asn	Val	Leu	Val	His	Leu	Lys	Pro	Val	Glu		
							40					45				

FIGURE 5

**Amino Acid
Sequence From
Fragment F2**

K E I P D D Y FVVLVGDMITTEALPTY Q T M L N T
 AAA GAA AUU CCN GAU GAU UAU CAA ACN AUG CUN AAU AC/N
 G G C C C G C

A

Forward Primers:

5'GCTAAGCTT AAP GAP ATQ CCA GAQ GAQ TA3' Desat 13-1
 A CCG Desat 13-2
 CCC Desat 13-3
 CCT Desat 13-4

**Reverse Primers:
(complements)**

Desat 13-5a 3' GTQ TGN TAC GAN TTP TGCTTAAGCGA
 Desat 13-6a AAQ

Oligonucleotides

P = A or G
 Q = T or C
 N = A, C, T or C

FIGURE 6

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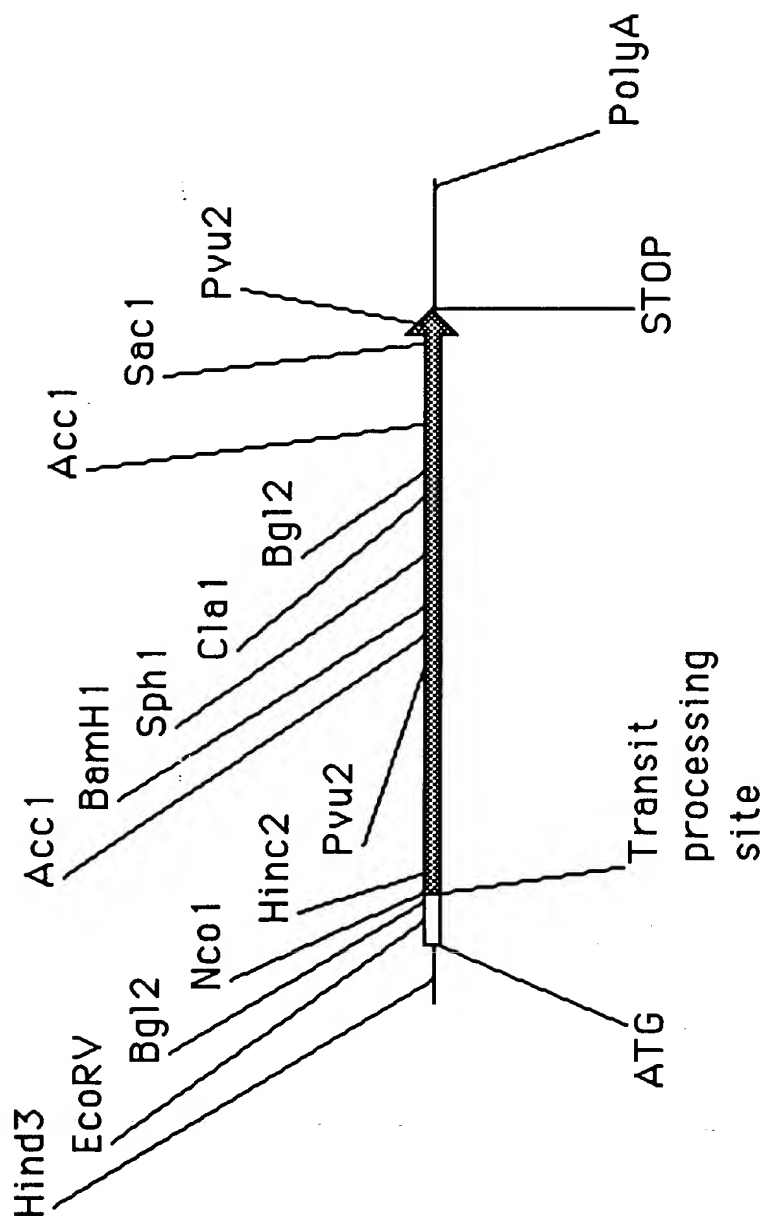


FIGURE 7A

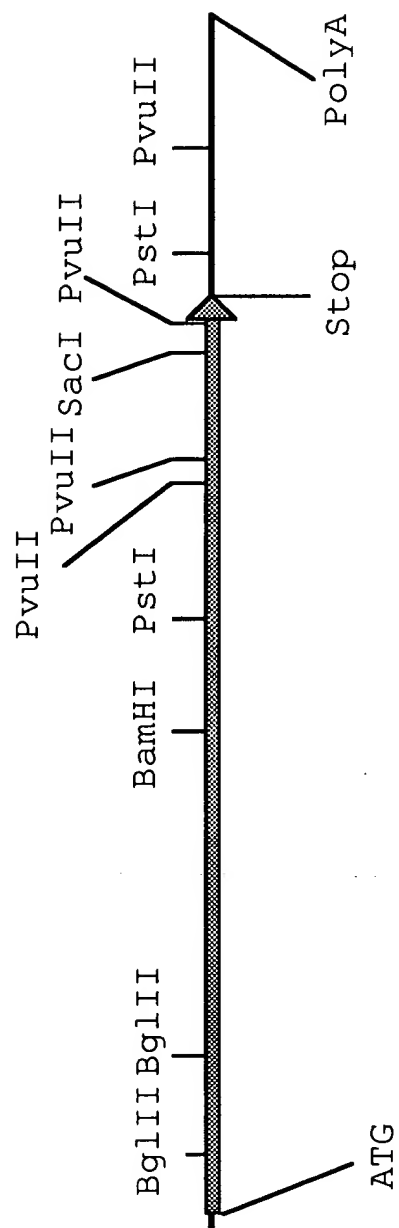


FIGURE 7B

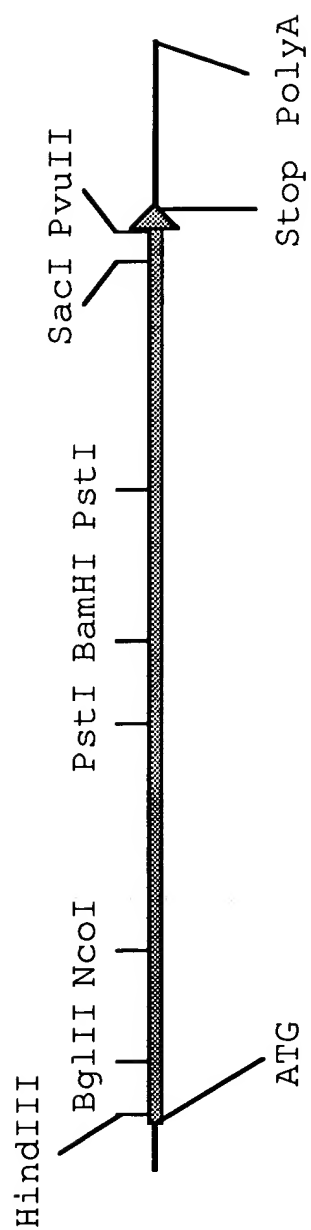


FIGURE 7C

TCTAGAAATC	TCTAATTACG	TCTGTTTGTT	CTATTTTTTA	TATGATATCA	AATATTCGTC	ATAAATATAT	70
GGTTTAAGAT	GCCAAAAAAT	TATTTACTTG	GTGAATATAA	TACGTTAAAT	ATTAGAAAATA	CATCATTTAG	140
TTAAATAAAT	AACCAAAAAC	CAAAAATTCA	TATCCGCGCT	GGCGGCGGGT	CAGGGTCTCG	TTAGTTTTAA	210
AATCAATGCA	GTTTACAATT	AATTTCCAGC	TGAAAATAAG	TATAATTGT	ATTGAAATTA	TAAAGTGACA	280
TTTTTTGTGT	AACAAATATT	TTGTGTAACA	AGAAATTAAAA	AAAAAAACAG	AAAATACTCA	GCTTTTTTAA	350
TAATAAAAAA	AATTAAATTGA	GTTAGAAAAAT	TGTTGTACCA	ATAACAAAAG	ATTTATATGG	AATTATAAAA	420
TCAACACACC	AATAACACAA	GACTTTTTTA	AAATTTAAGA	ATAATATAAG	CAATAACAAT	AGAATCTTCA	490
AATTCCTCAA	ATCCTTAAAA	ATCAATCTCC	CACTATTAAAT	CCCCCTTAGT	TTTAGTTGGT	AATGGCAACG	560
TTTGTTGACT	ACCGTATTGT	AACTTTTGTC	AAATTGTCAT	AAATACGTGT	CAAACCTCTGG	TAAAAAATTA	630
GTCTGCTACA	TCTGTCITTT	ATTTATAAAA	CACAGCTGTT	AATCAGAATT	TGGTTTATTA	AATCAACAAC	700
CTGCACGAAA	CTTGTGTGAG	CATATTTTGT	CTGTTTCTGG	TTCATGACCT	TCTTCCGCAT	GATGGCCAAG	770
TGTAATGGCC	ACTTGCAAGA	GCGTTTCTTC	AACGAGATAA	GTCGAACAAA	TATTTGTCCG	TTACGACCAC	840
ATATAAAATC	TCCCCATCTC	TATATATAAT	ACCAGCATTC	ACCATCATGA	ATACCTCAA	TCCCAATCTC	910
ACAAATACTT	CAATAAAAAG	ACCAAAAAAA	ATTAAAGCAA	AGAAAAGCCT	TCTTGTGCAC	AAAAAATAAA	980

FIGURE 8
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GAAGCCTTCT AGGTTTTCAC GAC ATG AAG TTC ACT ACT CTA ATG GTC ATC ACA TTG	1036
MET Lys Phe Thr Thr Thr Leu MET Val Ile Thr Leu	
GTG ATA ATC GCC ATC TCG TCT CCT GTT CCA ATT AGA GCA ACC ACG GTT GAA AGT	1090
Val Ile Ile Ala Ile Ser Ser Pro Val Pro Ile Arg Ala Thr Thr Val Glu Ser	
TTC GGA GAA GTG GCA CAA TCG TGT GTT GTG ACA GAA CTC GCC CCA TGC TTA CCA	1144
Phe Gly Glu Val Ala Gln Ser Cys Val Val Thr Glu Leu Ala Pro Cys Leu Pro	
GCA ATG ACC ACG GCA GGA GAC CCG ACT ACA GAA TGC TGC GAC AAA CTG GTA GAG	1198
Ala MET Thr Thr Ala Gly Asp Pro Thr Thr Glu Cys Cys Asp Lys Leu Val Glu	
CAG AAA CCA TGT CTT TGT GGT TAT ATT CGA AAC CCA GCC TAT AGT ATG TAT GTT	1252
Gln Lys Pro Cys Leu Cys Gly Tyr Ile Arg Asn Pro Ala Tyr Ser MET Tyr Val	
ACT TCT CCA AAC GGT CGC AAA GTC TTA GAT TTT TGT AAG GTT CCT TTT CCT AGT	1306
Thr Ser Pro Asn Gly Arg Lys Val Leu Asp Phe Cys Lys Val Pro Phe Pro Ser	
TGT TAAATCTCTC AAGACATTGC TAAGAAAAAT ATTATTAAAA ATAAAAGAAT CAAACTAGAT	1369
Cys	
CTGATGTAAC AATGAATCAT CATGTTATGG TTGAAGCTTA TATGCTGAAG TGTTTGATTT TATATATGTG	1439
TGTGTGTGTG TCCTGCTCAA TTTTGTGAAAC ACACACGTTT CTCCTGATTT GGATTAAAT TATATTTTGA	1509
GTAAAAAAA AGAAAAAGAT GGAATGCTAT TTATACAAAGT TGATGAAAAA GTGGAAGTAC AATTAGATA	1579

TCTCCTACAC	TTAAAGAATG	AAACAATAAT	AGACTTACGA	AACAAATGAA	AAATACATAA	ATTGTCGACA	1649
ATCAACGTCC	GATGACGAGT	TTATTATTAA	AAATTGTGT	GAAGGACTAG	CAGTTCAACC	AAATGATATT	1719
GAACATATAC	ATCAACAAAT	ATGATAATCA	TAAAAGAGAG	AATGGGGGGG	GGGTGTCGTT	TACCAGAAAC	1789
CTCTTTTCT	CAGCTCGCTA	AAACCCCTACC	ACTAGAGACC	TAGCTCTGAC	CGTCGGCTCA	TCGGTGCCGG	1859
AGGTGTAACC	TTTCTTTCCC	ATGACCCGAA	ACCTCTCTTT	CCCAACTCAC	GAAAACCCCTA	CAATCAAAAA	1929
CCTAGCTCCG	ACCGTCGGCT	CATCGGTGCC	GAAGGTGTAA	CCTTTCTCTC	CCATCATAGT	TTCTCGTAAA	1999
TGAAAGCTAA	TTGGGCAATC	GATTTTTTAA	TGTTTAAACC	ATGCCAAGCC	ATTTCTTATA	GGACAAATTGT	2069
CAATAATAGC	ATCTTTTGAG	TTTTGTCTCA	AAAGTGACAC	TAGAAGAAAA	AAGTCACAAA	AATGACATTTC	2139
ATTAAAAAGT	AAAATATCCC	TAATACCTTT	GGTTTAAATT	AAATAAGTAA	ACAAAAATAA	ATAAAAACAA	2209
ATAAAATAAA	AATAAAAAAT	GAAAAAAAGA	AATTTTTTAA	TAGTTTCAGA	TTATATGTTT	TCAGATTTCGA	2279
AATTTTTTAA	ATCCCTTTT	TTAAATTTTC	TTTTTTTGAAA	TTTTTTTTTT	TGAAATTTTT	TGAAACTGTT	2349
TTTAAAAATT	TTATTTTTAA	TTTTTTTAGTA	TTTATTTTTT	ATTTTATAAA	ATTTTAAACG	CTAATTCCAA	2419
AACTCCCCCC	CCCCCCCCCC	CCCCAATTCT	CTCCTAGTCT	TTTTCTCTTT	CTTATATTG	GGCTTCTATC	2489
TTCTCTTTTT	TTTTCAGGCC	CAAAGTATCA	TGTGTAACAA	CCGGTGTTCA	AAAACGCGCC	CGCCTGGCCG	2559

FIGURE 8

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TTTACTCGCC	CGATTAAATG	ATGATCGGAA	GGCTGCCATG	GCGAGGCGGA	GGTAATCAGT	GGTTCTAGGC	2629
GCTGAAACTA	GAAAACCTTC	AAAAATCGAA	ATTTTAAGAG	CTAAATCGGT	GTTTATCTCA	TGAATCTATT	2699
ATATTTAGTT	GAAACTCACA	AGAAATCGGTT	GTAATAACTA	TGAAATCGTG	CAAAAAAAAT	GAAGAACAAA	2769
ATATTCTCAG	ATCTGGAAAA	CACAGAGAAG	AGGTTGAAGA	TGAGGGTAAA	ATCGTATTTT	GTCATTCTTT	2839
AAACTAAAT	CAAAAAAAA	TGATGCAAAA	TTCAATGATA	ATAACTCGAA	CTCGCAACCA	TATGCATCTT	2909
TAGACTGCGA	CACGGACCAC	TAGACTAAGC	AATTTTAATG	TTTATTTCATC	ACAGACCCTAA	TATAATGTCTA	2979
AAACTAGGCG	CCGAGTACGC	CCCGCTTAAT	CCCGAGTTT	TGTTAGCTCG	CTAGACCCAG	GGTCACCGCC	3049
CGACTAACGA	GTAGCGTAAT	TCTGAACTGG	GGTAACAACA	TAGAGAACAT	CGCCGACCCCT	TCCCTGCCGA	3119
TGATGCCGCC	TCCGATGAAC	TTCTGTGAAC	GCCTTCAGTT	TCCATTGATT	TTCCCCCTTTA	ATCTGATCAG	3189
TTCCATGTTT	TATCCAACTC	ATCCCACTCC	GTAGCATTTA	ATCGATCTCA	TCATTTACAT	ACATAACCAG	3259
TAGGAGGTCT	CATATAAATT	TGAACGTTTC	CAGCGATGAA	CAGTGCCCAAT	CTCTGCGAAA	TCCATTTCTC	3329
TAAGCTCAGG	GCTGGCGGCT	GCAGCCCGGG	GATCCACTAG	TTCTAGGCGG	CCGCACCGCG	GTGGAGCTCC	3399
AATTCGCCCT	ATAGTGAGTC	GTATTACGCG	CGCTCACTGG	C			3440

XhoI

|

1 CTCGAGAGCTGAAGGATTTTGTTAGAGATTCAACGACAGATGGACCCCTTCCTCCACTAGGCAACTGC 69
2

70 AAGAACCTAACCAATGCAAATATCACTCCTCCTCAGCCCTTCAAGGAGCGTTAATAGGACTGGAACAAGCG 138

BglII

|

139 GTCAAGTGAGTAAATTTTCCTTCCAAGATAGATCTCTATGGTTCGGTTCATGAAGTTTGTGGTTAATT 207
169

208 GTGTAGCAACAGGATAGTGCAAGTGAGAATAGAGTTCGACCTCATCTACCTACCCCGGAACCTCTGAAT 276

277 GTATCCCCATTGAAGAAGAAGAGGGCAAATCCTGCACCCAGAAAGGATAAAGAAATTTTGGACGCCTGAA 345

346 GAAGTGGCAGTTCTGAGGGAAGGAGTAAAAGAGTATGTCTACTACTACTCTATAATCAAGTTTCAA 414

415 GAAGCTGAGCTTGGCTCTCAGTTTATATGTTTGTGTCAGGTATGTAATCATGGAAAAGAG 483

484 ATAAAGAATGCAAAACCCTGAAGTATTGGCAGAGAGGACTGAGGTGAGAGAGCATGTCACCTTTTGTGTTA 552

553 CTCATCTGAATTATCTTATATGCGAATTGTAAGTGGTACTAAAAGGTTTGTAACTTTTGGTAGGTGGAT 621

622 TTGAAGGATAAATGGAGGAACCTTGCTTCGGTAGCGGTAACAAGTTTATATGCTATGAAGTTTTTTG 690

691 CCTGCGTGACGTATCAGCAGCTGTGGAGAAGATGGTATTAGAAAGGGTCTTTTCACATTTTGTGTTGTG 759

FIGURE 9

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760 ACAAATATTAATTCGGCCGGTATGGTTTGGTTAAGACTTGTGAGAGACGTGTGGGGTTTTTTGATGTA 828
829 TAATTAGTCTGTGTTTAGAACGAAACAAGACTTGTGCGTATGCTTTTTTAACTTGAGGGGGTTTGT 897

BglII
|
898 GTTGTAGTTAGGAACCTTGACTTTGTCTCTTTCTCTCAAGATCTGATTGGTAAGGTCTGGGTGGTAGTA 966
937
967 CTGTTTGGTTTAAATTTTGGACTATTGAGTCACTGTGGCCCAATTGACTTTTAAATTAGGCTGGTATAT 1035
1036 TTTTGGTTTAAACCGGCTGAGATAGTGCAATTTTCGATTCAGTCAATTTTAAATTCTTCAAGGTAAT 1104
1105 GGGCTGAATACTTGTATAGTTTTTAAGACTTAAACAGGCCCTTAAAGGCCCATGTTATCATAAAACGTCAT 1173

HindIII
|
1174 TGTTAGAGTGCACCAAGCTTATAAAATGTAGCCAGGCCCTTAAAGACTTAAACAGGCCCTTAAAGACTT 1242
1190
1243 AACATTCCTTAAAGGCCCATGTTATCATAAAACGTCAATCGTTTTGAGTGCACCAAGCTAAATGTAGCC 1311
1312 AGGCCTTAAAGACTTAAACAGGCCCTTAAAGGCCCATGTTATCATAAAACGCCGCGTTTTGAGTGCAC 1380

HindIII

1381 CAAGCTTATAAATGTAGCCAGCTACCTCGGGACATCACGCTCTTTGTACACTCCGCCATCTCTCTCTCT 1449
1383

XhoI BglII

SalI

1450 CTCGAGCAGATCTCTCTCGGGAATATCGACAATGTTCGACCACTTTCTGCTCTTCCGCTCTCCATGCAAGC 1518
1451 1458 1484

1519 CACTTCTCTGTAATCTCATCTCCTTCTTGTGTTCCAGATCGCTCTGATCATACTTTCTTTAGATCA 1587

1588 TTTGCCCTCTGATCTGTTGCTTGATGTTTGAATCTCCACGCATGTTTGATTATGTTGAGAAATTAGAA 1656

1657 AAAAAATGTTAGCTTTACGAATCTTTAGTGATCATTTCAATTGGATTTCGAATCTTGTGTGACATTGA 1725

1726 GGCTTGTGTAGATTTCGATCTGTATTCAATTTGAATCACAGCTATAATAGTCATTTGAGTAGTAGTGT 1794

1795 TTAAATGAACATGTTTGTGTTGATGGAAACAAACAGGCAGCAACACGAGGATTAGTTTCCAGAA 1863

1864 GCCAGCTTTGGTTTCAACGACTAATCTCTCCTTCAACCTCCGCCGTTCAATCCCCACTCGTTTCTCAAT 1932

1933 CTCCTGCGCGGTAAGTTCTCATTTCTCAGCATTTAATTTTCGAGCTTGCTTGTCAATGGTACTCTCTCTAAT 2001

2002 GTCTATTTGGTTTATTAGGCCAAACCAGAGACGGTTGAGAAAGTGTCTAAGATAGTTAAGAACGAGCTA 2070

2071 TCACTCAAAGACGACCAAAAGGTCGTTGCCGGAGACCAAGTTTGCTGATCTTGGAGCAGATTCTCTCGAC 2139
 2140 ACTGTAAGTCATCAATCATCTCTTATGTGAATAAAGAGAACTTGAAGAGTTTGTGTTTAAACATATTAA 2208

 EcorV
 |
 2209 CTGAGTGTTTTGCGATGCAGGTTGAGATAGTAGTGGGTTTAGAGGAAAGAGTTTGATATCGAAAATGGCTGA 2277
 2264

 SstI
 |
 2278 AGAGAAAAGCTCAGAAAGATTGCTACTGTGGAGGAAGCTGCTGAACTCATTTGAAGAGCTCGTTCAACTTAA 2346
 2335

 2347 GAAGTAATTTTAGTATTAAGAGCAGCCAGGCTTTGTTGGGTTTGTGTTTTCATAAATCTTCCGTGCAT 2415
 2416 TTTCTTTTCTTTAATGTGTCAAGCGACTCTGTTGGTTTAAAGTAGTATCTGTTGCCATGGATCTCTC 2484

 SalI
 |
 HindIII
 |
 2485 TCTATTTGTCGACTGAAAACTTTTGGTTTACACATGAAAGCTTGTCTTGTCTTTCTTAAATCGAAAT 2553
 2493 2523

 2554 GCCAAATGCGAGATTAGGGAATCTTGTATTAAACACATACATAAAGTCAAAGAGTAGGCCCTAAGATGACA 2622
 2623 ATTTATAACAATCCTATTACACATTGTATATACAGGTTATGATTATCCCAATCAGCGTCAAAGAATCC 2691

FIGURE 9
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2692 AGCATCTTTCATCTCTGAATAGTAGACATTCTCCAAGTTCACATCTTCTCCTGCACCAAAAACCAGTA 2760
2761 CTAATCATGAACATTGCAATAATCACATGCCCTAGCGGAGAGTTTGGTGATGTGGTGTAGTGATAGT 2829
2830 GATACTGATGGTGCTAGAGCGGTTAAGAAAGGATTAACTGGAAAGTCTGCAAGGAAAGTAACATAGA 2898
2899 GAAGAGGAAGATAGGAGTGGTAACAAACACTTGTGATCCCCATACAGCCTCCCAGCATTTTTCAAAATGTT 2967
2968 ATTTCCCTTACATAAAGAAAACAAGAGAAGTCTGACTAGATGATATTTATATAGGATAAGTGTTTACCAT 3036
3037 AAGCCAAAGTGAGCGCCGTTTGCAAGAGCTAACCCAGACAGTACACGTTTGGCATAATATCTCATCAACAT 3105
3106 GATCTGAAAAGTAACATATCACAGTTAATGAACACAAATGGTTACCTTGAGAAAGCAAATCAAGACCCTATA 3174
3175 ACAAGCCCAGAGATGAGGAAAGTCCGTGTCAACGCTTCACCGCCATTTCGCCGTAGTTTCCTTGGAAAGACA 3243
3244 AAGGCCACCAACCAACTTACTTCCAGAAACAACACTCCAAATGTTGTCAACAAGTCAATAGATTCCA 3312
3313 AACTACTTCGTTACAGGGTTGTATAGATAATAATAAGTAAGTGGGAAGATAGTATAAAATAAAATAAA 3381
3382 TAAAAGATCCTATCGGTAAATAGTTTATAATATCGGGGCGTATATAAAGTATAAAAGAAACTCTTCTC 3450
3451 CAATCCGACCGTTGAAAATCACTCTCAATCTCTGGCGTAACGACCGGATCGTTCGCGCGTAATTTTCGC 3519
3520 TGCTATAAATAGAAACTTTCCCTCTTCTGTTTCTCGATCAAAAATTTTTTTTGGAAAAATTAAAGTTTGAA 3588

3589 TCTATCGTAGATGCTGTGACAAAAAATTGTTTATCGAAGATGAGAAACATGAGGCCTGTTTCATGC 3657

BamHI

|

3658 AAGGAACCAGACCCACGGATCCATCTTCGCCGATGATGACGTCTCCTCTGATGAATCGTCACGCACGGAC 3726
3674

BamHI

|

3727 AGGATCCCAACGCTGGACCAAGCATCTAACGCCAAGAAAGCACAGACGAAAGCAGCTCAGAGACTCGC 3795
3729

3796 GGCTGTGATGTCGAACCAACACAGGCGACGATGAAGACAGTGATGACCTTTCCTTTGACTACAACGC 3864

BglII

|

3865 TGTCGGAAGCATTGGTCTCGCTGCCCGGAAGATCT 3898
3894

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Lambda CGN1-2

NCG-186 Linear

LENGTH = 4325

```

      XhoI      SduI      NlaIV      HgiJII      HindIII
      |      |      |      |      |
1  CTCGAGGCAGTCACTAACATGAAGTTTGACGAGGAGCCCCAACTATGGGAAGCTTATTCTCTTTTCGAT 69
2
36
      XbaI      SacI
      |      |
70 ACTCTAATTGAGCCGTGCGCTCTATCTAGACCAATTAGAAATTGATGGAGCTCTAAAGTTGCTGGCTGT 138
95
121
      NdeI      SspI      NdeI
      |      |      |
139 TTTCTTGTTCATATGATTAACTTCTAAACTTGTGTATAAATATTCTCTGAAAGTGCTTCTTTTGGCATA 207
150
180
206
      Ksp632I
      |
208 TGTAGGTTGGGCAAAAACGAGGAAGATTGCTTCTCAATTGGAAGAGGATGAACAGCCGAAGAAGAAAA 276
245
```

FIGURE 10
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XhoI

|

277 TAAGAAATAGGCAGTCCTGCTACTCAATGGATCTCAGTCTATAACGGTCGTCGTCCCATGAAACAGAGGT 345
305

MmeI EcoRV

|

346 AAAACATTTTTGCGATATACACTTTGAAAGTTCCCTCACTAACTGTGTAATCTTTTGGTAGATATCACTA 414
401 408

SduI

MstI

BclI HgiAI

|

|

|

415 CAATGTCGGAGAGACAA3GGCTGMNCAATATACAAAAGGAAATGAAAGATGGCCCTTTTGTATTAGCTG 483
437 442
439

HaeI

|

469

SduI

HgiJII

|

484 TGTAGCATCAGCAGCTAATCTCTGGGCTCTCATCATGATGCTGGAACTGGATTCACTTCTCAAGTTA 552
512

FIGURE 10
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Cfr10I

BbvII

| |

553 TGAGTTGTCACCCGGTCTTCCTACACAAGGTAATAATCAGTTGAAGCAATTAAGAATCAATTGATTGT 621
560

563

622 AGTAAACTAAGAAGAACTTACCTTATGTTTCCCCGCAGGACTGGATTATGGAACAATGGGAAAAGAAC 690

SacI

|

691 TACTATATAAGCTCCATAGCTGGTTCAGATAACGGGAGCTCTTTAGTTGTTATGTCAAAAGGTTAGTGT 759
731

BbvII

|

760 TTAGTGAATAATAAACTTATACCCACAAAAGTCTTTCATTGACTTATTTATATACTTGTGTAATTGCTAG 828
782

829 GAACTACTTATTCTCAGCAGTCATACAAAAGTGAGTGACTCATTTCCGTTCAAAGTGGATAAAATAAGAAAT 897

898 GAAAAGAGATTTTCATGTAAACCTCCATGACAACTGCTGGTAATCGTTGGGGTGTGGTAATGTCGAGGA 966

BclI

|

967 ACTCTGGCTTCTCTGATCAGGTAGGTTTTTGTCTCTTATTGCTGCTGGTGTTTTATTTTCCCCCTGATAGT 1035
981

1036 CTAATATGATAAACTCTGCGTTGTGAAAAGGTGGTGGAGCTTGACTTTTGTACCCCAAGCGATGGGATAC 1104
 1105 ATAGGAGGTGGGAGAATGGGTATAGAATAACATCAATGGCAGCAACTGCGGATCAAGCAGCTTTCATAT 1173
 Tth111111
 |
 1174 TAAGCATACCAAAGCGTAAGATGGTGGATGAAACTCAAGAGACTCTCCGCACCACCGCCTTTCCAAAGTA 1242
 1175 1242
 ScaI
 |
 1243 CTCATGTCAAGGTGGTTTCTTTAGCTTTGAACACAGATTGGATCTTTTGTGTTTGTTCATATACT 1311
 1285
 XhoII
 |
 1312 TAGGACCTGAGAGCTTTTGGTTGATTTTTTTTCAGGACAAATGGGCGAAGAATCTGTACATTGCATCA 1380
 AflIII
 |
 1381 ATATGCTATGGCAGGACAGTGTGCTGATACACACTTAAAGCATCATGTGGAAAAGCCAAAGACAAATTGGAG 1449
 1415
 1450 CGAGACTCAGGGTCGTCATAATACCAATCAAAGACGTAAACCAGACGCAACCTCTTTGGTTGAATGTA 1518
 SspI
 |
 1519 ATGAAAGGGATGTGCTTGGTATGTATGTACGAATAACAAAAGAGAAGATGGAATTAGTAGTAAATA 1587
 1587

1588	TTTGGGAGCTTTTAAAGCCCTTCAAGTGIGCTTTTATCTTATGATATCATCCATTGGGTTGTTAA	1656	EcoRV
		1635	
1657	TGCGTCTCTAGATATGTTCCCTATATCTTCTCAGTGTCTGATAAGTGAAATGTGAGAAAACCATACCAA	1725	XbaI
		1664	
1726	ACCAAAATATTCAAATCTTATTTTAAATAATGTTGAATCACTCGGAGTTGCCACCTTCTGTGCCAATTG	1794	SspI
		1734	
1795	TGCTGAATCTATCACACTAGAAAAAACATTTCTCAAGGTAATGACTTGTGGACTATGTTCTGAATTC	1863	EcoRI
		1859	
1864	TCATTAAAGTTTTTATTTTCTGAAGTTTAAAGTTTTTACCTTCTGTGTTTGAATAATATCGTTTCATAAGATG	1932	Eco57I
		1904	

SphI
 NspI
 |
 1933 TCACGCCAGGACATGAGCTACACATCGCACATAGCATGCAGATCAGGACGATTTGTCACTCACTTCAAA 2001
 1971

 Tth111111
 |
 2002 CACCTAAGAGCTTCTCTCTCACAGCGCACACACATATGCATGCAATATTACACGATCGCCATGCAA 2070
 2015
 2037 2048 2053
 2036 2044 2056

 NdeI SphI NspI PmaCI
 [AvaIII] SspI AflIII
 || | | |
 2071 ATCTCCATTCTCACCTATAAATTAGAGCCTCGGCTTCACTCTTTACTCAAAACCAAACTCATCACTACA 2139
 2099

 Ksp632I
 |
 2140 GAACATACACAAATGGCGAACAAGCTCTTCCTCGTCTCGGCAACTCTCGCCTTGTTCCTTCTCACC 2208
 METAlaAsnLysLeuPheLeuValSerAlaThrLeuAlaLeuPheLeuLeuThr
 2171

SecI

|

2099

	SalI		HindII	NaeI	
		AccI	AccI	Cfr10I	
2209	AATGCCTCCGTCTACAGGACGGTTGTGAAGTCGACGAAAGATGATGCCACAATAATCCAGCGGCCCATTT	2277			
	AsnAlaSerValTyrArgThrValValGluValAspGluAspAlaThrAsnProAlaGlyProphe				
	2220	2241	2267		
		2242	2269		
		2240			
			Tthl111III		
			HindIII	NlaIV	
2278	AGGATTCCAATAATGTAGGAAGGAGTTTCAGCAAGCACACAACACTGAAAAGCTTGCCAACAATGGCTCCAC	2346			
	ArgileProLysCysArgLysGluPheGlnGlnAlaGlnHisLeuLysAlaCysGlnGlnTrpLeuHis				
		2325	2342		
				BbvII	
	Tthl111III	NlaIV			
2347	AAGCAGGCAATGCAGTCCGGTAGTGTCCTAAGCTGGACCCTCGATGGTGAGTTTGATTTTAAGACGAC	2415			
	LysGlnAlaMETGlnSerGlySerGlyProSerTrpThrLeuAspGlyGluPheAspPheGluAspAsp				
	2363	2384	2415		
			SacI	Ksp632	
	NlaIV				
	Apal	GsuI HaeI NspBII			
2416	GTGGAGAACCAACAACAGGGCCCCGACGAGAGGCCACCGCTGCTCCAGCAGTGCTGCAACGAGCTCCAC	2484			
	ValGluAsnGlnGlnGlyProGlnGlnArgProProLeuLeuGlnGlnCysCysAsnGluLeuHis				
	2438	2444 2449 2455	2481		
	2436		2484		

AccI

|

2830 TACTCCGTAGACGGTAATAAAGAGAGAAGTTTTTTTTTACTCTTGCTACTTTTCCCTATAAAGTGATGAT 2898
2838

SpeI
ScaI

|

VspI

|

2899 TAACAACAGATACACCCAAAAGAAAACAATTAAATCTATATTCAACAATGAAGCAGTACTAGTCTATTGAA 2967
2929
2954
2955

NspI

AflIII

|

2968 CATGTCAGATTTTCTTTTCTAAATGTCTAATTAAAGCCTTCAAGGCTAGTGATGATAAAGATCATCCA 3036
2968
2972

XhoII

NlaIV

BamHI

|

MmeI

BclI

|

3037 ATGGGATCCAAACAAGACTCAAATCTGGTTTTTGATCAGATACTTCAAAACTATTTTGTATTCATTAAA 3105
3041
3043

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	BbvII		Tth111
3106	TTATGCAAGTGTCTTTTATTGGTGAAGACTCTTTAGAAAGCAAGAACGACAGCAGTAATAAAAAA	3139	3174
		VspI	
3175	ACAAAGTTCAGTTTAAAGATTGTTATTGACTTATTGTCAATTGGAATAATAGTATGATATTAATATA	3237	3243
	Tth111111	VspI	
3244	GTTTTATTATATAATGCTTGCTATTCAAGATTGAGAACATTAATATGATACTGTCCACATATCCAA		3312
3250		3287	
	NdeI	Tth111111	
3313	TATATTAAGTTTCATTCTGTTCAAACATATGATAAGATGGTCAAAATGATTATGAGTTTGTATTAC	3341	3381
		3352	
	Eco57I	Eco57I	
3382	CTGAAGAAAAGATAAGTGAGCTTCGAGTTTCTGAAGGGTACGTGATCTTCATTTCTTGGCTAAAAGCGA	3404	3450
		3434	
3451	ATATGACATCACCTAGAGAAAGCCGATAATAGTAACTCTGTTCTTGGTTTTTGGTTTAATCAAACCGA		3519

EcoRV

|

3865 CCTTTGGTGGATATCGTGACGAAGGACCTCCCAGTGAAAGTCATTGGTTCTTACTCTTTTCTTAG 3933
3880

HindIII

AflII

|

3934 TCGAATCTTATTCTTGCTCTGCTCGTTGTTTTACCGATAAAGCTTAAAGACTTTATTGATAAAGTTCTCA 4002
3977
3974

4003 GCTTTGAATGTGAATGAACGTGTTCCCTGCTTATTAGTGTTCCCTTTGTTTGAAGTTGAATCACTGCTTA 4071

4072 GCACTTTTGTAGATTCACTCTTTGTGTTTAAAGTTAAAAGGTAGAAACTTTGTGACTTGTCTCCGTTATG 4140

HpaI

HindII

|

4141 ACAAGGTTAACTTTGTTGGTTATAACAGAAAGTTGCGACCTTTCTCCATGCTTGTGAGGGTGATGCTGTG 4209
4149

Tth111II

|

4179

XhoII

|

4210 GACCAAGCTCTCTCAGGCGGAAGATCCCTTACTTCAATGCCCCCAATCTACTTGGAAAAACAAGACACAGAT 4278
4231

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FIGURE 10